

mays=corn, Transposon Mutant, 150 nt]

Seq. No. 297846
Seq. ID LIB3150-050-Q1-N1-H11
Method BLASTX
NCBI GI g1885348
BLAST score 159
E value 3.0e-11
Match length 47
% identity 77
NCBI Description (X91515) histone H4 [Trichogramma caceociae]

Seq. No. 297847
Seq. ID LIB3150-050-Q1-N1-H9
Method BLASTX
NCBI GI g1346251
BLAST score 208
E value 2.0e-16
Match length 53
% identity 79
NCBI Description HISTONE H2B.4 >gi_577819_emb_CAA49585_ (X69961) H2B histone [Zea mays]

Seq. No. 297848
Seq. ID LIB3150-051-Q1-N1-B9
Method BLASTX
NCBI GI g1709000
BLAST score 422
E value 1.0e-41
Match length 88
% identity 92
NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi_960357_dbj_BAA09895_ (D63835) S-adenosylmethionine synthetase [Hordeum vulgare]

Seq. No. 297849
Seq. ID LIB3150-051-Q1-N1-C10
Method BLASTX
NCBI GI g133961
BLAST score 260
E value 1.0e-22
Match length 68
% identity 78
NCBI Description 40S RIBOSOMAL PROTEIN S4 (OMNIPOTENT SUPPRESSOR PROTEIN SUP44) (RP12) (S2E) >gi_70888_pir_R3BYS2 ribosomal protein S2.e - yeast (Saccharomyces cerevisiae) >gi_172793 (M59375) ribosomal protein S4 [Saccharomyces cerevisiae] >gi_1322683_emb_CAA96831_ (Z72645) ORF YGL123w [Saccharomyces cerevisiae] >gi_1628451_emb_CAA63835_ (X94106) SUP44 [Saccharomyces cerevisiae]

Seq. No. 297850
Seq. ID LIB3150-051-Q1-N1-C7
Method BLASTX
NCBI GI g3334756
BLAST score 224


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% identity      93
NCBI Description (AF030385) nitrate-induced NOI protein [Zea mays]
                  >gi_2895781 (AF045033) nitrate-induced NOI protein [Zea
                  mays]

Seq. No.        297906
Seq. ID         LIB3150-060-Q1-N1-H10
Method          BLASTX
NCBI GI         g1184776
BLAST score     151
E value         4.0e-10
Match length    58
% identity      47
NCBI Description (U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase
                  GAPC4 [Zea mays]

Seq. No.        297907
Seq. ID         LIB3150-061-Q1-N1-D1
Method          BLASTX
NCBI GI         g135398
BLAST score     272
E value         2.0e-34
Match length    94
% identity      76
NCBI Description TUBULIN ALPHA-1 CHAIN >gi_82731_pir_S15773 tubulin alpha-1
                  chain - maize >gi_22147_emb_CAA33734_ (X15704)
                  alphas-tubulin [Zea mays]

Seq. No.        297908
Seq. ID         LIB3150-063-P2-K1-A8
Method          BLASTN
NCBI GI         g1575127
BLAST score     92
E value         2.0e-44
Match length    136
% identity      92
NCBI Description Zea mays lumenal binding protein cBiPe2 mRNA, complete cds

Seq. No.        297909
Seq. ID         LIB3150-063-P2-K1-H6
Method          BLASTN
NCBI GI         g1037129
BLAST score     59
E value         8.0e-25
Match length    83
% identity      93
NCBI Description (gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize,
                  Tuxpeno CMS 450, mRNA Partial, 1889 nt]

Seq. No.        297910
Seq. ID         LIB3150-064-P1-N1-A5
Method          BLASTX
NCBI GI         g1708107
BLAST score     312
E value         1.0e-28
Match length    87
% identity      76

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Table 1. Demographic characteristics of the study population	
Age (years)	65.0 ± 1.5
Gender (male/female)	10/10
Education (years)	12.0 ± 1.0
Occupation (retired/employed)	10/10
Marital status (married/divorced/widowed)	10/0/0
Religion (Muslim/Jewish/Christian)	10/0/0
Smoking status (smoker/non-smoker)	10/0
Alcohol consumption (yes/no)	0/10
Family size (number of children)	2.5 ± 0.5
Income (USD/month)	1500 ± 200
Health insurance (yes/no)	10/0
Comorbidities (hypertension/diabetes/cholesterol)	5/3/2
Medication (yes/no)	10/0
Physical activity (yes/no)	10/0
Stress level (low/moderate/high)	10/0/0
Quality of life (SF-36 score)	45.0 ± 5.0
Life satisfaction (yes/no)	10/0
Overall health (good/fair/poor)	10/0/0
Life expectancy (years)	75.0 ± 2.0
Life expectancy (months)	900 ± 30
Life expectancy (days)	10800 ± 360
Life expectancy (hours)	259200 ± 8640
Life expectancy (minutes)	15552000 ± 518400
Life expectancy (seconds)	933120000 ± 31104000
Life expectancy (milliseconds)	93312000000 ± 3110400000
Life expectancy (microseconds)	9331200000000 ± 311040000000
Life expectancy (nanoseconds)	933120000000000 ± 31104000000000
Life expectancy (picoseconds)	93312000000000000 ± 3110400000000000
Life expectancy (femtoseconds)	933120000000000000 ± 311040000000000000
Life expectancy (attoseconds)	9331200000000000000 ± 3110400000000000000
Life expectancy (zeptoseconds)	93312000000000000000 ± 31104000000000000000
Life expectancy (yoctoseconds)	933120000000000000000 ± 311040000000000000000
Life expectancy (rattoseconds)	9331200000000000000000 ± 3110400000000000000000
Life expectancy (sextoseconds)	93312000000000000000000 ± 31104000000000000000000
Life expectancy (septoseconds)	933120000000000000000000 ± 311040000000000000000000
Life expectancy (octoseconds)	9331200000000000000000000 ± 3110400000000000000000000
Life expectancy (nonaseconds)	93312000000000000000000000 ± 31104000000000000000000000
Life expectancy (decaseconds)	933120000000000000000000000 ± 311040000000000000000000000
Life expectancy (centiseconds)	9331200000000000000000000000 ± 3110400000000000000000000000
Life expectancy (millesecseconds)	93312000000000000000000000000 ± 31104000000000000000000000000
Life expectancy (microseconds)	933120000000000000000000000000 ± 311040000000000000000000000000
Life expectancy (nanoseconds)	9331200000000000000000000000000 ± 3110400000000000000000000000000
Life expectancy (picoseconds)	93312000000000000000000000000000 ± 31104000000000000000000000000000
Life expectancy (femtoseconds)	933120000000000000000000000000000 ± 311040000000000000000000000000000
Life expectancy (attoseconds)	9331200000000000000000000000000000 ± 3110400000000000000000000000000000
Life expectancy (zeptoseconds)	93312000000000000000000000000000000 ± 31104000000000000000000000000000000
Life expectancy (yoctoseconds)	933120000000000000000000000000000000 ± 311040000000000000000000000000000000
Life expectancy (rattoseconds)	9331200000000000000000000000000000000 ± 3110400000000000000000000000000000000
Life expectancy (sextoseconds)	93312000000000000000000000000000000000 ± 31104000000000000000000000000000000000
Life expectancy (septoseconds)	933120000000000000000000000000000000000 ± 311040000000000000000000000000000000000
Life expectancy (octoseconds)	9331200000000000000000000000000000000000 ± 3110400000000000000000000000000000000000
Life expectancy (nonaseconds)	93312000000000000000000000000000000000000 ± 31104000000000000000000000000000000000000
Life expectancy (decaseconds)	933120000000000000000000000000000000000000 ± 311040000000000000000000000000000000000000
Life expectancy (centiseconds)	9331200000000000000000000000000000000000000 ± 3110400000000000000000000000000000000000000
Life expectancy (millesecseconds)	93312000000000000000000000000000000000000000 ± 31104000000000000000000000000000000000000000
Life expectancy (microseconds)	9331200 ± 3110400
Life expectancy (nanoseconds)	93312000 ± 31104000
Life expectancy (picoseconds)	9331200 ± 3110400
Life expectancy (femtoseconds)	93312000 ± 31104000
Life expectancy (attoseconds)	9331200 ± 3110400
Life expectancy (zeptoseconds)	93312000 ±

Seq. No.	297920
Seq. ID	LIB3150-065-P2-K1-B10
Method	BLASTN
NCBI GI	g3851000
BLAST score	151
E value	2.0e-79
Match length	267
% identity	90
NCBI Description	Zea mays pyruvate dehydrogenase E1 beta subunit isoform 2 mRNA, nuclear gene encoding mitochondrial protein, complete cds

Method BLASTX
 NCBI GI g82512
 BLAST score 171
 E value 2.0e-12
 Match length 37
 % identity 47
 NCBI Description ubiquitin precursor - rice (fragment)
 >gi_218189_dbj_BAA02241_ (D12776) poly-ubiquitin [Oryza
 sativa]

Seq. No. 297937
 Seq. ID LIB3150-067-P1-N1-G4
 Method BLASTN
 NCBI GI g22176
 BLAST score 163
 E value 1.0e-86
 Match length 289
 % identity 89
 NCBI Description Z.mays P gene

Seq. No. 297938
 Seq. ID LIB3150-067-P2-K1-A6
 Method BLASTX
 NCBI GI g2511531
 BLAST score 197
 E value 9.0e-16
 Match length 49
 % identity 73
 NCBI Description (AF008120) alpha tubulin 1 [Eleusine indica]
 >gi_3163944_emb_CAA06618_ (AJ005598) alpha-tubulin 1
 [Eleusine indica]

Seq. No. 297939
 Seq. ID LIB3150-067-P2-K1-B12
 Method BLASTN
 NCBI GI g2286150
 BLAST score 151
 E value 3.0e-79
 Match length 331
 % identity 85
 NCBI Description Zea mays translation initiation factor (eIF-4A) mRNA,
 complete cds

Seq. No. 297940
 Seq. ID LIB3150-067-P2-K1-D4
 Method BLASTN
 NCBI GI g168482
 BLAST score 95
 E value 3.0e-46
 Match length 159
 % identity 91
 NCBI Description Corn starch branching enzyme II mRNA, complete cds

Seq. No. 297941
 Seq. ID LIB3150-067-P2-K1-D6
 Method BLASTN
 NCBI GI g2668741

BLAST score 165
E value 7.0e-88
Match length 248
% identity 92
NCBI Description Zea mays glycine-rich RNA binding protein (GRP) mRNA, complete cds

Seq. No. 297942
Seq. ID LIB3150-067-P2-K1-F3
Method BLASTX
NCBI GI g1172836
BLAST score 169
E value 3.0e-12
Match length 46
% identity 76
NCBI Description GTP-BINDING NUCLEAR PROTEIN RAN-B1 >gi_496272 (L16787) small ras-related protein [Nicotiana tabacum]

Seq. No. 297943
Seq. ID LIB3150-067-P2-K1-G2
Method BLASTX
NCBI GI g4096786
BLAST score 168
E value 7.0e-12
Match length 35
% identity 94
NCBI Description (U39958) NADP-malic enzyme [Zea mays]

Seq. No. 297944
Seq. ID LIB3150-068-P1-N1-B6
Method BLASTX
NCBI GI g4467099
BLAST score 221
E value 4.0e-18
Match length 72
% identity 71
NCBI Description (AL035538) glycine hydroxymethyltransferase like protein [Arabidopsis thaliana]

Seq. No. 297945
Seq. ID LIB3150-068-P1-N1-C2
Method BLASTX
NCBI GI g1184774
BLAST score 271
E value 5.0e-24
Match length 74
% identity 78
NCBI Description (U45856) cytosolic glyceraldehyde-3-phosphate dehydrogenase GAPC3 [Zea mays]

Seq. No. 297946
Seq. ID LIB3150-068-P1-N1-C5
Method BLASTX
NCBI GI g1709619
BLAST score 280
E value 5.0e-25
Match length 57

Seq. No. 297961
 Seq. ID LIB3150-069-P2-K1-C11
 Method BLASTN
 NCBI GI g1037129
 BLAST score 58
 E value 4.0e-24
 Match length 86
 % identity 92
 NCBI Description (gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize, Tuxpeno CMS 450, mRNA Partial, 1889 nt]

Seq. No. 297962
 Seq. ID LIB3150-069-P2-K1-D8
 Method BLASTN
 NCBI GI g22272
 BLAST score 80
 E value 4.0e-37
 Match length 167
 % identity 87
 NCBI Description Maize mRNA for enolase (2-phospho-D-glycerate hydrolase)

Seq. No. 297963
 Seq. ID LIB3150-069-P2-K1-F2
 Method BLASTX
 NCBI GI g567890
 BLAST score 153
 E value 5.0e-10
 Match length 129
 % identity 38
 NCBI Description (L37352) beta-galactosidase-complementation protein [Cloning vector]

Seq. No. 297964
 Seq. ID LIB3150-069-P2-K1-F4
 Method BLASTX
 NCBI GI g135417
 BLAST score 225
 E value 1.0e-18
 Match length 74
 % identity 66
 NCBI Description TUBULIN ALPHA-3 CHAIN >gi_100946_pir_JN0105 tubulin alpha-3 chain - maize >gi_22150_emb_CAA44861_ (X63176) Alpha-tubulin #3 [Zea mays] >gi_485377 (M60171) alpha-3 tubulin [Zea mays]

Seq. No. 297965
 Seq. ID LIB3150-069-P2-K1-G9
 Method BLASTX
 NCBI GI g464706
 BLAST score 156
 E value 2.0e-10
 Match length 43
 % identity 77
 NCBI Description 40S RIBOSOMAL PROTEIN S15 (S12) >gi_1078669_pir_A53793 ribosomal protein S12, cytosolic - Podospora anserina >gi_401841_emb_CAA80805_ (Z23267) cytoplasmic ribosomal protein S12 [Podospora anserina]



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Variable	Mean	SD	Min	Max
Age	34.5	10.2	21	55
Gender	1.2	0.4	1	2
Marital status	1.5	0.5	1	3
Education	12.5	1.5	9	16
Occupation	1.8	0.8	1	4
Income	1.5	0.5	1	3
Health status	1.2	0.4	1	2
Stress level	2.5	1.0	1	4
Life satisfaction	3.5	1.5	1	5
Work-life balance	2.8	1.2	1	4
Family support	1.8	0.8	1	3
Community support	1.5	0.5	1	3
Healthcare access	1.2	0.4	1	2
Quality of life	3.8	1.8	1	5
Overall well-being	3.2	1.5	1	5
Physical health	3.5	1.5	1	5
Mental health	3.0	1.5	1	5
Social health	3.5	1.5	1	5
Environmental health	3.5	1.5	1	5
Healthcare quality	3.5	1.5	1	5
Healthcare cost	3.5	1.5	1	5
Healthcare access	3.5	1.5	1	5
Healthcare quality	3.5	1.5	1	5
Healthcare cost	3.5	1.5	1	5
Healthcare access	3.5	1.5	1	5
Healthcare quality	3.5	1.5	1	5
Healthcare cost	3.5	1.5	1	5
Healthcare access	3.5	1.5	1	5
Healthcare quality	3.5	1.5	1	5
Healthcare cost	3.5	1.5	1	5
Healthcare access	3.5	1.5	1	5
Healthcare quality	3.5	1.5	1	5
Healthcare cost	3.5	1.5	1	5
Healthcare access	3.5	1.5	1	5
Healthcare quality	3.5	1.5	1	5
Healthcare cost	3.5	1.5	1	5
Healthcare access	3.5	1.5	1	5
Healthcare quality	3.5	1.5	1	5
Healthcare cost	3.5	1.5	1	5
Healthcare access	3.5	1.5	1	5
Healthcare quality	3.5	1.5	1	5
Healthcare cost	3.5	1.5	1	5
Healthcare access	3.5	1.5	1	5
Healthcare quality	3.5	1.5	1	5
Healthcare cost	3.5	1.5	1	5
Healthcare access	3.5	1.5	1	5
Healthcare quality	3.5	1.5	1	5
Healthcare cost	3.5	1.5	1	5
Healthcare access	3.5	1.5	1	5
Healthcare quality	3.5	1.5	1	5
Healthcare cost	3.5	1.5	1	5
Healthcare access	3.5	1.5	1	5
Healthcare quality	3.5	1.5	1	5
Healthcare cost	3.5	1.5	1	5
Healthcare access	3.5	1.5	1	5
Healthcare quality	3.5	1.5	1	5
Healthcare cost	3.5	1.5	1	5
Healthcare access	3.5	1.5	1	5
Healthcare quality	3.5	1.5	1	5
Healthcare cost	3.5	1.5	1	5
Healthcare access	3.5	1.5	1	5
Healthcare quality	3.5	1.5	1	5
Healthcare cost	3.5	1.5	1	5
Healthcare access	3.5	1.5	1	5
Healthcare quality	3.5	1.5	1	5
Healthcare cost	3.5	1.5	1	5
Healthcare access	3.5	1.5	1	5
Healthcare quality	3.5	1.5	1	5
Healthcare cost	3.5	1.5	1	5
Healthcare access	3.5	1.5	1	5
Healthcare quality	3.5	1.5	1	5
Healthcare cost	3.5	1.5	1	5
Healthcare access	3.5	1.5	1	5
Healthcare quality	3.5	1.5	1	5
Healthcare cost	3.5	1.5	1	5
Healthcare access	3.5	1.5	1	5
Healthcare quality	3.5	1.5	1	5
Healthcare cost	3.5	1.5	1	5
Healthcare access	3.5	1.5	1	5
Healthcare quality	3.5	1.5	1	5
Healthcare cost	3.5	1.5	1	5
Healthcare access	3.5	1.5	1	5
Healthcare quality	3.5	1.5	1	5
Healthcare cost	3.5	1.5	1	5
Healthcare access	3.5			

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BLAST score 165
E value 1.0e-11
Match length 41
% identity 66
NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No. 297987
Seq. ID LIB3150-073-P1-N1-G5
Method BLASTX
NCBI GI g3608481
BLAST score 272
E value 3.0e-24
Match length 68
% identity 75
NCBI Description (AF088913) ribosomal protein L27a [Petunia x hybrida]

Seq. No. 297988
Seq. ID LIB3150-073-P2-K1-A1
Method BLASTN
NCBI GI g644491
BLAST score 56
E value 8.0e-23
Match length 152
% identity 85
NCBI Description Corn mRNA for elongation factor 1A

Seq. No. 297989
Seq. ID LIB3150-073-P2-K1-A11
Method BLASTX
NCBI GI g1172816
BLAST score 194
E value 7.0e-15
Match length 70
% identity 60
NCBI Description 60S RIBOSOMAL PROTEIN L11A (L16A) >gi_624938_emb_CAA57395_
(X81799) ribosomal protein L16 [Arabidopsis thaliana]

Seq. No. 297990
Seq. ID LIB3150-073-P2-K1-A7
Method BLASTX
NCBI GI g136063
BLAST score 261
E value 9.0e-23
Match length 53
% identity 100
NCBI Description TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
>gi_68426_pir_ISZMT triose-phosphate isomerase (EC
5.3.1.1) - maize >gi_168647 (L00371) triosephosphate
isomerase 1 [Zea mays] >gi_217974_dbj_BAA00009_ (D00012)
triosephosphate isomerase [Zea mays]

Seq. No. 297991
Seq. ID LIB3150-073-P2-K1-A9
Method BLASTX
NCBI GI g1172874
BLAST score 145
E value 5.0e-09

000101-91048950

Method	BLASTN
NCBI GI	g22324
BLAST score	71
E value	1.0e-31
Match length	151
% identity	87
NCBI Description	Z.mays mRNA for H2B histone (clone CH2B221)
Seq. No.	297997
Seq. ID	LIB3150-073-P2-K1-F11
Method	BLASTN
NCBI GI	g602605
BLAST score	72
E value	3.0e-32
Match length	254
% identity	63
NCBI Description	Zea mays tandem genes for alpha1-tubulin and alpha2-tubulin
Seq. No.	297998
Seq. ID	LIB3150-074-P1-N1-D2
Method	BLASTX
NCBI GI	g1321661
BLAST score	186
E value	3.0e-14
Match length	52
% identity	71
NCBI Description	(D45423) ascorbate peroxidase [Oryza sativa]
Seq. No.	297999
Seq. ID	LIB3150-074-P1-N1-E2
Method	BLASTX
NCBI GI	g3126967
BLAST score	358
E value	1.0e-34
Match length	99
% identity	14
NCBI Description	(AF061807) polyubiquitin [Elaeagnus umbellata]
Seq. No.	298000
Seq. ID	LIB3150-074-P1-N1-F12
Method	BLASTN
NCBI GI	g642120
BLAST score	48
E value	3.0e-18
Match length	76
% identity	91
NCBI Description	Oryza sativa small GTP-binding protein (ORRab-2) mRNA, complete cds
Seq. No.	298001
Seq. ID	LIB3150-074-P1-N1-H6
Method	BLASTX
NCBI GI	g2144183
BLAST score	156
E value	5.0e-11
Match length	53
% identity	53

NCBI GI	g22272
BLAST score	99
E value	2.0e-48
Match length	205
% identity	88
NCBI Description	Maize mRNA for enolase (2-phospho-D-glycerate hydrolase)
Seq. No.	298037
Seq. ID	LIB3150-077-P2-N2-E2
Method	BLASTN
NCBI GI	g1808693
BLAST score	132
E value	5.0e-68
Match length	224
% identity	90
NCBI Description	S.stapfianus pSD.34 mRNA
Seq. No.	298038
Seq. ID	LIB3150-077-P2-N2-E5
Method	BLASTX
NCBI GI	g118104
BLAST score	547
E value	3.0e-56
Match length	121
% identity	87
NCBI Description	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE) (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN) >gi_68408_pir_CSZM peptidylprolyl isomerase (EC 5.2.1.8) -maize >gi_168461 (M55021) cyclophilin [Zea mays] >gi_829148_emb_CAA48638_ (X68678) cyclophilin [Zea mays]
Seq. No.	298039
Seq. ID	LIB3150-077-P2-N2-E6
Method	BLASTX
NCBI GI	g1185556
BLAST score	159
E value	2.0e-11
Match length	37
% identity	92
NCBI Description	(U45859) glyceraldehyde-3-phosphate dehydrogenase [Zea mays]
Seq. No.	298040
Seq. ID	LIB3150-077-P2-N2-F9
Method	BLASTN
NCBI GI	g1037129
BLAST score	191
E value	1.0e-103
Match length	219
% identity	65
NCBI Description	(gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize, Tuxpeno CMS 450, mRNA Partial, 1889 nt]
Seq. No.	298041
Seq. ID	LIB3150-077-P2-N2-G9
Method	BLASTX
NCBI GI	q2865661

NCBI Description T.aestivum L mRNA for histone H2B

Seq. No. 298057
 Seq. ID LIB3150-079-P1-N1-A11
 Method BLASTX
 NCBI GI g113621
 BLAST score 163
 E value 3.0e-11
 Match length 68
 % identity 57

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME
 >gi_68196_pir_ADZM fructose-bisphosphate aldolase (EC
 4.1.2.13), cytosolic - maize >gi_168420 (M16220) aldolase
 [Zea mays] >gi_295850_emb_CAA31366_ (X12872) fructose
 bisphosphate aldolase [Zea mays] >gi_225624_prf_1307278A
 cytoplasmic aldolase [Zea mays]

Seq. No. 298058
 Seq. ID LIB3150-079-P1-N1-A8
 Method BLASTX
 NCBI GI g232029
 BLAST score 238
 E value 3.0e-20
 Match length 70
 % identity 70

NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
 >gi_100154_pir_S21989 translation elongation factor eEF-1
 alpha chain - carrot >gi_18339_emb_CAA42843_ (X60302)
 elongation factor 1A [Daucus carota]

Seq. No. 298059
 Seq. ID LIB3150-079-P1-N1-D2
 Method BLASTX
 NCBI GI g2760349
 BLAST score 232
 E value 9.0e-20
 Match length 68
 % identity 14

NCBI Description (U84969) ubiquitin [Arabidopsis thaliana]

Seq. No. 298060
 Seq. ID LIB3150-079-P1-N1-E2
 Method BLASTX
 NCBI GI g1184776
 BLAST score 405
 E value 2.0e-39
 Match length 78
 % identity 95

NCBI Description (U45857) cytosolic glyceraldehyde-3-phosphate dehydrogenase
 GAPC4 [Zea mays]

Seq. No. 298061
 Seq. ID LIB3150-079-P1-N1-E3
 Method BLASTX
 NCBI GI g4510368
 BLAST score 276
 E value 2.0e-24

[illegible]

Seq. No.	298073
Seq. ID	LIB3150-081-P2-N2-D11
Method	BLASTN
NCBI GI	g168425
BLAST score	186
E value	1.0e-100
Match length	255
% identity	93
NCBI Description	Zea mays brittle-1 protein (bt1) mRNA, complete cds

Seq. No.	298075
Seq. ID	LIB3150-082-P1-N1-A5
Method	BLASTX
NCBI GI	g168586
BLAST score	147
E value	7.0e-10
Match length	43
% identity	70
NCBI Description	(M58656) pyruvate,orthophosphate dikinase [Zea mays]

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cds

Seq. No. 298109
 Seq. ID LIB3150-087-P2-K1-G2
 Method BLASTN
 NCBI GI g22121
 BLAST score 191
 E value 1.0e-103
 Match length 243
 % identity 95
 NCBI Description Maize alcohol dehydrogenase 1 gene (Adh1-1F)

Seq. No. 298110
 Seq. ID LIB3150-088-P2-K1-A4
 Method BLASTN
 NCBI GI g22272
 BLAST score 105
 E value 7.0e-52
 Match length 328
 % identity 82
 NCBI Description Maize mRNA for enolase (2-phospho-D-glycerate hydrolase)

Seq. No. 298111
 Seq. ID LIB3150-088-P2-K1-B10
 Method BLASTX
 NCBI GI g3928086
 BLAST score 157
 E value 2.0e-10
 Match length 45
 % identity 58
 NCBI Description (AC005770) unknown protein [Arabidopsis thaliana]

Seq. No. 298112
 Seq. ID LIB3150-088-P2-K1-D11
 Method BLASTX
 NCBI GI g4586035
 BLAST score 147
 E value 3.0e-10
 Match length 89
 % identity 48
 NCBI Description (AC007109) putative prohibitin protein [Arabidopsis thaliana]

Seq. No. 298113
 Seq. ID LIB3150-088-P2-K1-F2
 Method BLASTX
 NCBI GI g4115937
 BLAST score 226
 E value 2.0e-18
 Match length 51
 % identity 75
 NCBI Description (AF118223) contains similarity to human PCF11p homolog (GB:AF046935) [Arabidopsis thaliana]

Seq. No. 298114
 Seq. ID LIB3150-089-P1-N1-B10
 Method BLASTX



```
Seq. No.      298130
Seq. ID      LIB3150-091-P1-N1-F1
Method       BLASTN
NCBI GI      g2431768
BLAST score   64
E value      2.0e-27
Match length  160
% identity    85
NCBI Description Zea mays acidic ribosomal protein Pl1a (rppla) mRNA,
                complete cds
```

```
Seq. No.      298131
Seq. ID      LIB3150-091-P1-N1-G4
Method       BLASTX
NCBI GI      g3236242
BLAST score   176
E value      8.0e-13
Match length  100
% identity    45
NCBI Description (AC004684) putative ribosomal protein L36 [Arabidopsis
thaliana]
```

```
Seq. No.      298132
Seq. ID      LIB3150-091-P1-N1-G7
Method       BLASTX
NCBI GI      g1174613
BLAST score   162
E value      1.0e-14
Match length  84
% identity    57
NCBI Description  26S PROTEASE REGULATORY SUBUNIT 6A HOMOLOG (TAT-BINDING
PROTEIN HOMOLOG 1) (TBP-1) >gi_556560_dbj_BAA04614_
(D17788) rice homologue of Tat binding protein [Oryza
sativa]
```

```
Seq. No.      298133
Seq. ID      LIB3150-092-P1-N1-B1
Method       BLASTX
NCBI GI      g462243
BLAST score   208
E value      1.0e-16
Match length  85
% identity    61
NCBI Description HISTONE H4 >gi_421921_pir_S32769 histone H4 - tomato
                >gi_297150_emb_CAA48923_ (X69179) histone H4 [Lycopersicon
                esculentum] >gi_297152_emb_CAA48924_ (X69180) histone H4
                [Lycopersicon esculentum] >gi_2746721_ (AF038387) histone H4
                [Capsicum annuum]
```

Seq. No.	298134
Seq. ID	LIB3150-092-P1-N1-B4
Method	BLASTX
NCBI GI	g461498
BLAST score	227
E value	8.0e-19


```

Match length      92
% identity        58
NCBI Description  ALANINE AMINOTRANSFERASE 2 (GPT) (GLUTAMIC--PYRUVIC
                  TRANSAMINASE 2) (GLUTAMIC--ALANINE TRANSAMINASE 2)
                  (ALAAT-2) >gi_320619_pir_S28429 alanine transaminase (EC
                  2.6.1.2) - proso millet >gi_296204_emb_CAA49199_ (X69421)
                  alanine aminotransferase [Panicum miliaceum]

```

```
Seq. No.      298135
Seq. ID      LIB3150-092-P1-N1-C3
Method       BLASTX
NCBI GI      g627584
BLAST score   168
E value      6.0e-12
Match length  114
% identity    34
NCBI Description protein p84 - human >gi_550058 (L36529) protein p84 [Homo sapiens]
```

```
Seq. No.      298136
Seq. ID      LIB3150-092-P1-N1-D8
Method       BLASTX
NCBI GI      g1174867
BLAST score   151
E value      1.0e-11
Match length  71
% identity    58
NCBI Description  UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX UBIQUINONE-BINDING
PROTEIN QP-C (UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 8.2
KD PROTEIN) >gi_633687_emb_CAA55862_ (X79275)
ubiquinol--cytochrome c reductase [Solanum tuberosum]
>gi_1094912_prf_2107179A cytochrome c
oxidase:SUBUNIT=8.2kd [Solanum tuberosum]
```

```
Seq. No.      298137
Seq. ID      LIB3150-092-P2-K1-A4
Method       BLASTN
NCBI GI      g168492
BLAST score   35
E value      3.0e-10
Match length  39
% identity    97
NCBI Description  Corn histone H3 (H3C3) gene, complete cds
```

Seq. No.	298138
Seq. ID	LIB3150-092-P2-K1-D12
Method	BLASTN
NCBI GI	g1321660
BLAST score	47
E value	2.0e-17
Match length	71
% identity	92
NCBI Description	Rice mRNA for ascorbate peroxidase, complete cds

Seq. No.	298139
Seq. ID	LIB3150-092-P2-K1-E1
Method	BLASTN

[illegible]

```
Seq. No.      298167
Seq. ID      LIB3150-095-P1-N1-E1
Method       BLASTN
NCBI GI      g1037129
BLAST score   296
E value      1.0e-166
Match length  400
% identity    94
NCBI Description (gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize,
Tuxpeno CMS 450, mRNA Partial, 1889 nt]
```


BLAST score	220
E value	1.0e-120
Match length	267
% identity	96
NCBI Description	Z.mays (cv DH5xDH7) hsp70-5 mRNA for heat shock protein

Seq. No.	298230
Seq. ID	LIB3150-107-P2-K1-B10
Method	BLASTX
NCBI GI	g2492519
BLAST score	161
E value	6.0e-11
Match length	43
% identity	77
NCBI Description	26S PROTEASE REGULATORY SUBUNIT 7 (26S PROTEASOME SUBUNIT 7) >gi_1395191_dbj_BAA13021_ (D86121) 26S proteasome ATPase subunit [Spinacia oleracea]

Seq. No.	298231
Seq. ID	LIB3150-107-P2-K1-B5
Method	BLASTN
NCBI GI	g498772
BLAST score	143
E value	1.0e-74
Match length	252
% identity	89
NCBI Description	Z.mays (cv DH5xDH7) hsp70-4 mRNA for heat shock protein

Seq. No.	298232
Seq. ID	LIB3150-107-P2-K1-F12
Method	BLASTN
NCBI GI	g2341060
BLAST score	181
E value	3.0e-97
Match length	285
% identity	91
NCBI Description	Zea mays translational initiation factor eIF-4A (tif-4A3) mRNA, complete cds

Seq. No.	298233
Seq. ID	LIB3150-107-P2-K1-H2
Method	BLASTN
NCBI GI	g22324
BLAST score	172
E value	6.0e-92
Match length	212
% identity	95
NCBI Description	Z.mays mRNA for H2B histone (clone cH2B221)

Seq. No.	298234
Seq. ID	LIB3150-108-P1-N1-A11
Method	BLASTX
NCBI GI	g1658313
BLAST score	148
E value	2.0e-09
Match length	102
% identity	39

NCBI Description (Y08987) osr40g2 [Oryza sativa]

```
Seq. No.      298235
Seq. ID      LIB3150-108-P1-N1-C4
Method       BLASTX
NCBI GI      g419803
BLAST score   347
E value      1.0e-32
Match length  122
% identity    60
NCBI Description  zein protein - maize >gi_168705 (M72708) zein protein [Zea mays]
```

```
Seq. No.      298236
Seq. ID      LIB3150-108-P1-N1-C5
Method       BLASTX
NCBI GI      g168664
BLAST score   317
E value      2.0e-29
Match length  65
% identity    88
NCBI Description (M13507) zein protein precursor [Zea mays]
```

Seq. No.	298237
Seq. ID	LIB3150-108-P1-N1-E2
Method	BLASTX
NCBI GI	g3335372
BLAST score	172
E value	3.0e-12
Match length	122
% identity	38
NCBI Description	(AC003028) putative SRG1 protein [Arabidopsis thaliana]

```
Seq. No.          298238
Seq. ID           LIB3150-108-P1-N1-E5
Method            BLASTX
NCBI GI           g1658313
BLAST score       321
E value           8.0e-30
Match length      91
% identity        34
NCBI Description   (Y08987) osr40g2 [Oryza sativa]
```

```
Seq. No.      298239
Seq. ID      LIB3150-108-P1-N1-G2
Method       BLASTX
NCBI GI      g3746936
BLAST score   175
E value      3.0e-13
Match length  69
% identity    54
NCBI Description (AF091808) actin 1 [Anemia phyllitidis]
```

Seq. No. 298240
Seq. ID LIB3150-108-P1-N1-H7
Method BLASTX
NCBI GI q2282584

(gpc3) mRNA, complete cds

Seq. No. 298246
Seq. ID LIB3150-109-P2-K1-A4
Method BLASTX
NCBI GI g2827700
BLAST score 200
E value 2.0e-15
Match length 84
% identity 49
NCBI Description (AL021684) DEAD box ATP dependent helicase protein
[Arabidopsis thaliana]

Seq. No. 298247
Seq. ID LIB3150-109-P2-K1-B5
Method BLASTX
NCBI GI g4309698
BLAST score 307
E value 4.0e-28
Match length 130
% identity 56
NCBI Description (AC006266) putative glucosyltransferase [Arabidopsis
thaliana]

Seq. No. 298248
Seq. ID LIB3150-109-P2-K1-D12
Method BLASTN
NCBI GI g22272
BLAST score 98
E value 1.0e-47
Match length 287
% identity 86
NCBI Description Maize mRNA for enolase (2-phospho-D-glycerate hydrolase)

Seq. No. 298249
Seq. ID LIB3150-109-P2-K1-E6
Method BLASTN
NCBI GI g168505
BLAST score 41
E value 5.0e-14
Match length 45
% identity 98
NCBI Description Zea mays histone H3 gene, complete cds

Seq. No. 298250
Seq. ID LIB3150-109-P2-K1-F10
Method BLASTX
NCBI GI g1169533
BLAST score 335
E value 3.0e-31
Match length 81
% identity 85
NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
(2-PHOSPHO-D-GLYCERATE HYDRO-LYASE)
>gi_515827_emb_CAA56645_ (X80474) enolase [Neocallimastix
frontalis]

Method BLASTN
 NCBI GI g168694
 BLAST score 59
 E value 1.0e-24
 Match length 125
 % identity 94
 NCBI Description Maize gamma zein mRNA, partial cds

Seq. No. 298273
 Seq. ID LIB3150-116-P2-K1-B8
 Method BLASTX
 NCBI GI g1706323
 BLAST score 217
 E value 2.0e-17
 Match length 114
 % identity 45
 NCBI Description ORNITHINE DECARBOXYLASE (ODC) >gi_2118242_pir_S64704
 ornithine decarboxylase (EC 4.1.1.17) - jimsonweed
 >gi_871008_emb_CAA61121_ (X87847) ornithine decarboxylase
 [Datura stramonium]

Seq. No. 298274
 Seq. ID LIB3150-116-P2-K1-G5
 Method BLASTN
 NCBI GI g1895083
 BLAST score 34
 E value 1.0e-09
 Match length 86
 % identity 85
 NCBI Description Zea mays golgi associated protein se-wap41 mRNA, complete
 cds

Seq. No. 298275
 Seq. ID LIB3150-117-P2-K1-B7
 Method BLASTX
 NCBI GI g2642446
 BLAST score 154
 E value 3.0e-10
 Match length 51
 % identity 65
 NCBI Description (AC002391) similar to auxin-responsive GH3 protein
 [Arabidopsis thaliana]

Seq. No. 298276
 Seq. ID LIB3150-117-P2-K1-F8
 Method BLASTN
 NCBI GI g2104711
 BLAST score 41
 E value 6.0e-14
 Match length 69
 % identity 90
 NCBI Description Zea mays endosperm specific protein mRNA, complete cds

Seq. No. 298277
 Seq. ID LIB3150-117-P2-K1-G4
 Method BLASTN
 NCBI GI g998429


```

BLAST score      193
E value          1.0e-104
Match length     289
% identity       92
NCBI Description Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21
                  (sz22-21) gene, complete cds; retrotransposon Opie-2 gag
                  protein, polyprotein, and copia protein genes, complete
                  cds; and unknown genes

```

Seq. No.	298292
Seq. ID	LIB3151-001-P1-K1-E4
Method	BLASTX
NCBI GI	g1172977
BLAST score	217
E value	1.0e-17
Match length	92
% identity	50
NCBI Description	60S RIBOSOMAL PROTEIN L18 >gi_606970 (U15741) cytoplasmic ribosomal protein L18 [Arabidopsis thaliana]

Seq. No.	298293
Seq. ID	LIB3151-001-P1-K1-E7
Method	BLASTX
NCBI GI	g2832243
BLAST score	180
E value	2.0e-13
Match length	74
% identity	55
NCBI Description	(AF031569) 22-kDa alpha zein 4 [Zea mays]

Seq. No.	298294
Seq. ID	LIB3151-001-P1-K1-F2
Method	BLASTN
NCBI GI	g22549
BLAST score	238
E value	1.0e-131
Match length	278
% identity	97
NCBI Description	Maize gene for a 27kDa storage protein, zein

```
Seq. No.      298295
Seq. ID      LIB3151-001-P1-K1-F4
Method       BLASTX
NCBI GI      g168695
BLAST score   157
E value      2.0e-10
Match length  89
% identity    46
NCBI Description (M16218) gamma zein [Zea mays] >gi_225315_prf__1211356A
              zein gamma [Zea mays]
```

Seq. No.	298296
Seq. ID	LIB3151-001-P1-K1-F7
Method	BLASTN
NCBI GI	g168681
BLAST score	102
E value	4.0e-50


```

Method                BLASTX
NCBI GI                g121472
BLAST score            257
E value                3.0e-22
Match length           110
% identity              45
NCBI Description        GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
                        (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
                        >gi_72326_pir_ZM19 glutelin 2 precursor (clone pME119) -
                        maize >gi_22289_emb_CAA26149_ (X02230) glutelin-2 precursor
                        [Zea mays] >gi_22517_emb_CAA37594_ (X53514) zein Zc2 [Zea
                        mays] >gi_168485 (M16066) glutelin-2 [Zea mays]

```

Seq. No.	298307
Seq. ID	LIB3151-002-P1-K1-D1
Method	BLASTN
NCBI GI	g168679
BLAST score	40
E value	4.0e-13
Match length	56
% identity	93
NCBI Description	Maize 19 kDa zein mRNA, clone cZ19C2, complete cds. >gi 270687 qb I03334 Sequence 9 from Patent US

```
Seq. No.          298308
Seq. ID           LIB3151-002-P1-K1-E2
Method            BLASTX
NCBI GI           g2832246
BLAST score       367
E value           4.0e-35
Match length      124
% identity        66
NCBI Description   (AF031569) 22-kDa alpha zein 8 [Zea mays]
```

```
Seq. No.      298309
Seq. ID       LIB3151-002-P1-K1-E3
Method        BLASTX
NCBI GI       g121472
BLAST score   184
E value       1.0e-13
Match length  80
% identity    49
NCBI Description  GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
                (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
                >gi_72326_pir_ZMZM19 glutelin 2 precursor (clone pME119) -
                maize >gi_22289_emb_CAA26149_ (X02230) glutelin-2 precursor
                [Zea mays] >gi_22517_emb_CAA37594_ (X53514) zein Zc2 [Zea
                mays] >gi_168485 (M16066) glutelin-2 [Zea mays]
```

```
Seq. No.      298310
Seq. ID      LIB3151-002-P1-K1-E5
Method       BLASTX
NCBI GI      g16073
BLAST score   369
E value       2.0e-35
Match length  109
% identity    70
```


NCBI Description (X59526) zein protein [Acetabularia mediterranea]

```
Seq. No.      298311
Seq. ID      LIB3151-002-P1-K1-G1
Method       BLASTN
NCBI GI      g22215
BLAST score   70
E value      4.0e-31
Match length  312
% identity    84
NCBI Description  Z.mays ZSF4C1 gene for zein
```

```
Seq. No.      298312
Seq. ID      LIB3151-002-P1-K1-G5
Method       BLASTX
NCBI GI      g2146739
BLAST score   227
E value      1.0e-18
Match length  69
% identity    65
NCBI Description hexokinase (EC 2.7.1.1) 1 - Arabidopsis thaliana >gi_881521
                (U28214) hexokinase 1 [Arabidopsis thaliana]
```

```
Seq. No.      298313
Seq. ID      LIB3151-002-P1-K1-G6
Method       BLASTX
NCBI GI      g168699
BLAST score   236
E value      7.0e-20
Match length  68
% identity    74
NCBI Description (M60836) zein [Zea mays]
```

```
Seq. No.          298314
Seq. ID           LIB3151-002-P1-K1-H2
Method            BLASTX
NCBI GI           g168701
BLAST score       276
E value           1.0e-24
Match length      96
% identity        65
NCBI Description   (M60837) zein [Zea mays]
```

Seq. No.	298315
Seq. ID	LIB3151-002-P1-K1-H7
Method	BLASTN
NCBI GI	g168425
BLAST score	180
E value	9.0e-97
Match length	252
% identity	93
NCBI Description	Zea mays brittle-1 protein (bt1) mRNA, complete cds

```
Seq. No.      298316
Seq. ID      LIB3151-003-Q1-K1-A10
Method      BLASTX
NCBI GI      q2832247
```



```
% identity      55
NCBI Description HMG1/2-LIKE PROTEIN >gi_541981_pir__S39556 HMG protein -
                 fava bean
```

```
Seq. No.      298332
Seq. ID      LIB3151-003-Q1-K1-E6
Method       BLASTX
NCBI GI      g141605
BLAST score   364
E value      6.0e-35
Match length  93
% identity    83
NCBI Description  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
                >gi_72312_pir_ZIZM92 19K zein precursor (clone cz19C2) -
                maize >gi_168680 (M12145) 19 kDa zein protein [Zea mays]
```

```
Seq. No.      298333
Seq. ID      LIB3151-003-Q1-K1-F12
Method       BLASTX
NCBI GI      g4586031
BLAST score   280
E value      6.0e-25
Match length  64
% identity   83
NCBI Description (AC007109) unknown protein [Arabidopsis thaliana]
```

Seq. No.	298334
Seq. ID	LIB3151-003-Q1-K1-F5
Method	BLASTN
NCBI GI	g168484
BLAST score	285
E value	1.0e-159
Match length	373
% identity	95
NCBI Description	Maize endosperm glutelin-2 gene, complete cds

Seq. No.	298335
Seq. ID	LIB3151-003-Q1-K1-G4
Method	BLASTN
NCBI GI	g22326
BLAST score	35
E value	3.0e-10
Match length	82
% identity	87
NCBI Description	Z.mays gene for Hageman factor inhibitor

```
Seq. No.          298336
Seq. ID           LIB3151-003-Q1-K1-G7
Method            BLASTX
NCBI GI           g168699
BLAST score       169
E value           3.0e-12
Match length      82
% identity        51
NCBI Description  (M60836) zein [Zea mays]
```

Seq. No. 298337


```

Match length      125
% identity        51
NCBI Description  zein Zd1, 19K - maize >gi_535020_emb_CAA47639_ (X67203)
                  zein Zd1 (19 kDa zein) [Zea mays]

```

```
Seq. No.      298363
Seq. ID      LIB3151-005-Q1-K1-E12
Method       BLASTX
NCBI GI      g266398
BLAST score   349
E value      4.0e-33
Match length  96
% identity    68
NCBI Description TRYPsin/FACTOR XIIIA INHIBITOR PRECURSOR (HAGEMAN FACTOR
INHIBITOR) (CHFI) >gi_68849_pir_TIZM1 trypsin/factor XIIa
inhibitor precursor - maize >gi_22327_emb_CAA37998_
(X54064) corn Hageman factor inhibitor [Zea mays]
```

```
Seq. No.      298364
Seq. ID      LIB3151-005-Q1-K1-E5
Method       BLASTX
NCBI GI      g141608
BLAST score   316
E value      3.0e-29
Match length  118
% identity    60
NCBI Description  ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi_100943_pir_S15655
zein, 19K - maize >gi_22446_emb_CAA37651_ (X53582) 19 kDa
zein [Zea mays]
```

```
Seq. No.          298365
Seq. ID           LIB3151-005-Q1-K1-E8
Method            BLASTX
NCBI GI           g168701
BLAST score       169
E value           5.0e-12
Match length      53
% identity        58
NCBI Description   (M60837) zein [Zea mays]
```

```
Seq. No.      298366
Seq. ID       LIB3151-005-Q1-K1-E9
Method        BLASTX
NCBI GI       g719291
BLAST score   197
E value       2.0e-15
Match length  83
% identity    46
NCBI Description (U19134) unknown [Arabidopsis thaliana]
               >qi_1095007_prf_2107236A_SABRE_gene [Arabidopsis thaliana]
```

```
Seq. No.      298367
Seq. ID      LIB3151-005-Q1-K1-F1
Method       BLASTN
NCBI GI      g1037129
BLAST score   349
E value      0.0e+00
```



```
BLAST score      351
E value         2.0e-33
Match length    112
% identity      67
NCBI Description 22K zein precursor (clone pZ22.3) - maize >gi_168686
                  (J01246) 26.99 kd zein protein [Zea mays]
```

```
Seq. No.          298373
Seq. ID           LIB3151-005-Q1-K1-H11
Method            BLASTX
NCBI GI           g141597
BLAST score       221
E value           1.0e-32
Match length      130
% identity        62
NCBI Description   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
                  >gi_72314_pir_ZIZM3 19K zein precursor (clone A30) - maize
                  >gi_22545_emb_CAA24728_ (V01481) reading frame zein [2]
                  [Zea mays]
```

```
Seq. No.          298374
Seq. ID           LIB3151-006-Q1-K1-B2
Method            BLASTX
NCBI GI           g141610
BLAST score       184
E value           1.0e-13
Match length      51
% identity        75
NCBI Description   ZEIN-ALPHA PRECURSOR (CLONE Z4)
```

```
Seq. No.      298375
Seq. ID      LIB3151-006-Q1-K1-C3
Method       BLASTX
NCBI GI      g168664
BLAST score   282
E value      2.0e-25
Match length  94
% identity    60
NCBI Description (M13507) zein protein precursor [Zea mays]
```

```
Seq. No.      298376
Seq. ID      LIB3151-006-Q1-K1-C6
Method       BLASTX
NCBI GI      g141617
BLAST score   271
E value      8.0e-24
Match length  66
% identity    77
NCBI Description  ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
>gi_100941_pir_S12140 zein Zc1 - maize
>gi_100945_pir_B29017 zein 2 - maize
>gi_22515_emb_CAA37595_(X53515) zein Zc1 [Zea mays]
>gi_168666_(M16460) 16-kDa zein protein [Zea mays]
```

Seq. No.	298377
Seq. ID	LIB3151-006-Q1-K1-C9
Method	BLASTX

Seq. No.	298393
Seq. ID	LIB3151-007-Q1-K1-C11
Method	BLASTX
NCBI GI	g141605
BLAST score	177
E value	4.0e-13
Match length	71
% identity	54
NCBI Description	ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2) >gi_72312_pir_ZIZM92 19K zein precursor (clone cZ19C2) - maize >gi_168680 (M12145) 19 kDa zein protein [Zea mays]
Seq. No.	298394
Seq. ID	LIB3151-007-Q1-K1-C12
Method	BLASTN
NCBI GI	g22516
BLAST score	160
E value	8.0e-85
Match length	312
% identity	88
NCBI Description	Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)
Seq. No.	298395
Seq. ID	LIB3151-007-Q1-K1-C2
Method	BLASTX
NCBI GI	g141597
BLAST score	230
E value	2.0e-27
Match length	119
% identity	60
NCBI Description	ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30) >gi_72314_pir_ZIZM3 19K zein precursor (clone A30) - maize >gi_22545_emb_CAA24728_ (V01481) reading frame zein [2] [Zea mays]
Seq. No.	298396
Seq. ID	LIB3151-007-Q1-K1-C5
Method	BLASTX
NCBI GI	g419803
BLAST score	162
E value	6.0e-16
Match length	109
% identity	46
NCBI Description	zein protein - maize >gi_168705 (M72708) zein protein [Zea mays]
Seq. No.	298397
Seq. ID	LIB3151-007-Q1-K1-D11
Method	BLASTN
NCBI GI	g22514
BLAST score	69
E value	6.0e-31
Match length	125
% identity	89
NCBI Description	Maize Zc1 gene for Zein Zc1 (14 kD zein-2)

NCBI Description Maize ATP2 mRNA for mitochondrial ATP synthase beta subunit

Seq. No. 298435
 Seq. ID LIB3151-010-Q1-K1-F2
 Method BLASTN
 NCBI GI g168665
 BLAST score 208
 E value 1.0e-113
 Match length 236
 % identity 97
 NCBI Description Maize 16-kDa zein-2 mRNA, complete cds

Seq. No. 298436
 Seq. ID LIB3151-010-Q1-K1-F9
 Method BLASTX
 NCBI GI g419803
 BLAST score 285
 E value 1.0e-25
 Match length 110
 % identity 53
 NCBI Description zein protein - maize >gi_168705 (M72708) zein protein [Zea mays]

Seq. No. 298437
 Seq. ID LIB3151-010-Q1-K1-G1
 Method BLASTX
 NCBI GI g100938
 BLAST score 200
 E value 8.0e-16
 Match length 84
 % identity 56
 NCBI Description zein precursor - maize >gi_22442_emb_CAA32513_ (X14335)
 zein precursor (AA -21 to 90) [Zea mays]

Seq. No. 298438
 Seq. ID LIB3151-010-Q1-K1-G10
 Method BLASTX
 NCBI GI g16073
 BLAST score 182
 E value 2.0e-13
 Match length 101
 % identity 46
 NCBI Description (X59526) zein protein [Acetabularia mediterranea]

Seq. No. 298439
 Seq. ID LIB3151-010-Q1-K1-H7
 Method BLASTN
 NCBI GI g22516
 BLAST score 287
 E value 1.0e-160
 Match length 329
 % identity 97
 NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)

Seq. No. 298440
 Seq. ID LIB3151-011-Q1-K1-A11
 Method BLASTN

BLAST score 68
E value 3.0e-30
Match length 87
% identity 94
NCBI Description Zea mays zein protein gene, complete cds

Seq. No. 298457
Seq. ID LIB3151-012-Q1-K1-C12
Method BLASTX
NCBI GI g141604
BLAST score 415
E value 1.0e-40
Match length 132
% identity 71
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C1)
>gi_72310_pir_ZIZM91 19K zein precursor (clone cZ19C1) -
maize >gi_168678 (M12146) 19 kDa zein protein [Zea mays]

Seq. No. 298458
Seq. ID LIB3151-012-Q1-K1-C6
Method BLASTX
NCBI GI g224507
BLAST score 173
E value 1.0e-19
Match length 93
% identity 61
NCBI Description zein A1 [Zea mays]

Seq. No. 298459
Seq. ID LIB3151-012-Q1-K1-D12
Method BLASTN
NCBI GI g168677
BLAST score 34
E value 6.0e-10
Match length 50
% identity 94
NCBI Description Maize 19 kDa zein mRNA, clone cZ19C1, complete cds

Seq. No. 298460
Seq. ID LIB3151-012-Q1-K1-D3
Method BLASTX
NCBI GI g141617
BLAST score 229
E value 5.0e-19
Match length 100
% identity 51
NCBI Description ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
>gi_100941_pir_S12140 zein Zc1 - maize
>gi_100945_pir_B29017 zein 2 - maize
>gi_22515_emb_CAA37595 (X53515) zein Zc1 [Zea mays]
>gi_168666 (M16460) 16-kDa zein protein [Zea mays]

Seq. No. 298461
Seq. ID LIB3151-012-Q1-K1-D6
Method BLASTN
NCBI GI g168484
BLAST score 192

